



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/516,728A

DATE: 04/21/2004

TIME: 08:01:00

Input Set : D:\1242-12-2 CIP.ST25.txt

Output Set: N:\CRF4\04212004\I516728A.raw

3 <110> APPLICANT: VANDERBILT UNIVERSITY
 4 DANIEL, THOMAS
 5 TAKAHASHI, TAKAMUNE
 6 MERNAUGH, RAYMOND
 8 <120> TITLE OF INVENTION: MODULATION OF ENDOTHELIAL CELL SURFACE RECEPTOR ACTIVITY IN THE
 9 REGULATION OF ANGIOGENESIS
 11 <130> FILE REFERENCE: 1242/12/2 CIP
 13 <140> CURRENT APPLICATION NUMBER: 09/516,728A
 14 <141> CURRENT FILING DATE: 2000-03-01
 16 <150> PRIOR APPLICATION NUMBER: US 09/152,160
 17 <151> PRIOR FILING DATE: 1998-09-10
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 8
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
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 31 1 5
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 4
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Artificial
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Artifical peptide spacer
 42 <400> SEQUENCE: 2
 44 Leu Ala Leu Ala
 45 1
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 5117
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Homo sapiens
 54 <220> FEATURE:
 55 <221> NAME/KEY: CDS
 56 <222> LOCATION: (350)..(4363)
 58 <300> PUBLICATION INFORMATION:
 59 <301> AUTHORS: Ostman,A., Yang,Q. and Tonks,N.K.
 60 <302> TITLE: Expression of DEP-1, a receptor-like
 61 protein-tyrosine-phosphatase, is enhanced with increasing cell
 62 density
 63 <303> JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 64 <304> VOLUME: 91

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65 <305> ISSUE: 21
 66 <306> PAGES: 9680-9684
 67 <307> DATE: 1994-10-11
 68 <308> DATABASE ACCESSION NO: U10886
 69 <309> DATABASE ENTRY DATE: 1994-06-15
 70 <313> RELEVANT RESIDUES: (1)..(5117)
 72 <400> SEQUENCE: 3

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75	gccgcgcgt	gggggtggc	gccgctcgct	ccgcccgcg	aagccctgc	gcgcgtcagg	120
77	acgcggcccc	cccgccgcag	ccgcgtcagg	ctccggcgtg	tggccgcggc	cgccgcgcg	180
79	ctgcatgtc	tccggcaag	ccggggcggg	cggagcgggg	acgaggcgg	ccggctggcg	240
81	gaggaggagg	cgaaggagac	ggcaggaggc	ggcagacgac	gtgcccggc	tcgggcgcac	300
83	ggcgccccc	gattcgcgcg	tccggggcac	gttccaggc	gcgcggggc	atg aag ccg	358
84						Met Lys Pro	
85						1	
87	gcg gcg	cg	gag	gcg	cg	ctg	406
88	Ala Ala	Arg Glu	Ala Arg	Leu Pro	Pro Arg	Gly Leu	
89	5	10	15				
91	g	cg	cc	ct	ct	ct	454
92	Ala Leu	Pro Leu	Leu Leu	Leu Leu	Arg Leu	Gly Gln Ile	
93	20	25	30	35			
95	gca ggt	ggc acc	cct agt	cca att	cct gac	cct tca	502
96	Ala Gly	Gly Thr	Pro Ser	Pro Ile	Pro Asp	Pro Ser	
97	40	45	50				
99	gcc aca	ggg gaa	aat ggc	ata acg	cag atc	agt aca	550
100	Ala Thr	Gly Glu	Asn Gly	Ile Thr	Gln Ile	Ser Ser	
101	55	60	65				
103	ttt cat	aaa cag	aat gga	act gga	aca cct	cag gtg	598
104	Phe His	Lys Gln	Asn Gly	Thr Gly	Thr Pro	Gln Val	
105	70	75	80				
107	agt gag	gat ggt	gaa agc	tct gga	gcc aac	gat agt	646
108	Ser Ser	Glu Asp	Gly Gly	Ser Ser	Gly Ala	Asn Asp	
109	85	90	95				
111	gaa caa	gga tct	aat ggg	act gat	ggg gca	tct caa	694
112	Glu Gln	Gly Ser	Asn Gly	Thr Asp	Gly Ala	Ser Gln	
113	100	105	110	115			
115	agc act	ggg ccc	agt cct	gtg ttt	gac att	aaa gct	742
116	Ser Thr	Gly Pro	Ser Pro	Val Phe	Asp Ile	Lys Ala	
117	120	125	130				
119	cca acc	aat gtg	atc tta	act tgg	aaa agt	aat gac	790
120	Pro Thr	Asn Val	Ile Leu	Thr Trp	Lys Ser	Asn Asp	
121	135	140	145				
123	gag tac	aag tat	gta gta	aag cat	aag atg	gaa aat	838
124	Glu Tyr	Lys Tyr	Val Val	Lys His	Lys Met	Glu Asn	
125	150	155	160				
127	act gtt	gtg cat	caa cca	tgg tgt	aac atc	aca ggc	886
128	Thr Val	Val His	Gln Pro	Trp Cys	Asn Ile	Thr Gly	
129	165	170	175				
131	act tca	tat gta	ttc tcc	atc act	cca gga	ata ggc	934
						aat gag	
						act tgg	

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132	Thr Ser Tyr Val Phe Ser Ile Thr Pro Gly Ile Gly Asn Glu Thr Trp				
133	180	185	190	195	
135	gga gat ccc aga gtc ata aaa gtc atc aca gag ccg atc cca gtt tct		982		
136	Gly Asp Pro Arg Val Ile Lys Val Ile Thr Glu Pro Ile Pro Val Ser				
137	200	205	210		
139	gat ctc cgt gtt gcc ctc acg ggt gtg agg aag gct gtc tcc tgg		1030		
140	Asp Leu Arg Val Ala Leu Thr Gly Val Arg Lys Ala Ala Leu Ser Trp				
141	215	220	225		
143	agc aat ggc aat ggc acc gcc tcc tgc cgg gtt ctt ctt gaa agc att		1078		
144	Ser Asn Gly Asn Gly Thr Ala Ser Cys Arg Val Leu Leu Glu Ser Ile				
145	230	235	240		
147	gga agc cat gag gag ttg actcaa gac tca aga ctt cag gtc aat atc		1126		
148	Gly Ser His Glu Glu Leu Thr Gln Asp Ser Arg Leu Gln Val Asn Ile				
149	245	250	255		
151	tcg gac ctg aag cca ggg gtt caa tac aac atc aac ccg tat ctt cta		1174		
152	Ser Asp Leu Lys Pro Gly Val Gln Tyr Asn Ile Asn Pro Tyr Leu Leu				
153	260	265	270	275	
155	caa tca aat aag aca aag gga gac ccc ttg ggc aca gaa ggt ggc ttg		1222		
156	Gln Ser Asn Lys Thr Lys Gly Asp Pro Leu Gly Thr Glu Gly Gly Leu				
157	280	285	290		
159	gat gcc agc aat aca gag aga agc cgg gca ggg agc ccc acc gcc cct		1270		
160	Asp Ala Ser Asn Thr Glu Arg Ser Arg Ala Gly Ser Pro Thr Ala Pro				
161	295	300	305		
163	gtg cat gag tcc ctc gtg gga cct gtg gac cca tcc tcc ggc cag		1318		
164	Val His Asp Glu Ser Leu Val Gly Pro Val Asp Pro Ser Ser Gly Gln				
165	310	315	320		
167	cag tcc cga gac acg gaa gtc ctg ctt gtc ggg tta gag cct ggc acc		1366		
168	Gln Ser Arg Asp Thr Glu Val Leu Val Gly Leu Glu Pro Gly Thr				
169	325	330	335		
171	cga tac aat gcc acc gtt tat tcc caa gca gcg aat ggc aca gaa gga		1414		
172	Arg Tyr Asn Ala Thr Val Tyr Ser Gln Ala Ala Asn Gly Thr Glu Gly				
173	340	345	350	355	
175	cag ccc cag gcc ata gag ttc agg aca aat gct att cag gtt ttt gac		1462		
176	Gln Pro Gln Ala Ile Glu Phe Arg Thr Asn Ala Ile Gln Val Phe Asp				
177	360	365	370		
179	gtc acc gct gtg aac atc agt gcc aca agc ctg acc ctg atc tgg aaa		1510		
180	Val Thr Ala Val Asn Ile Ser Ala Thr Ser Leu Thr Leu Ile Trp Lys				
181	375	380	385		
183	gtc agc gat aac gag tcg tca tct aac tat acc tac aag ata cat gtg		1558		
184	Val Ser Asp Asn Glu Ser Ser Asn Tyr Thr Tyr Lys Ile His Val				
185	390	395	400		
187	gct ggg gag aca gat tct tcc aat ctc aac gtc agt gag cct cgc gct		1606		
188	Ala Gly Glu Thr Asp Ser Ser Asn Leu Asn Val Ser Glu Pro Arg Ala				
189	405	410	415		
191	gtc atc ccc gga ctc cgc tcc agc acc ttc tac aac atc aca gtg tgt		1654		
192	Val Ile Pro Gly Leu Arg Ser Ser Thr Phe Tyr Asn Ile Thr Val Cys				
193	420	425	430	435	
195	cct gtc cta ggt gac atc gag ggc acg ccg ggc ttc ctc caa gtg cac		1702		
196	Pro Val Leu Gly Asp Ile Glu Gly Thr Pro Gly Phe Leu Gln Val His				

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197	440	445	450	
199	acc ccc cct gtt cca gtt tct gac ttc cga gtg aca gtg gtc agc acg			1750
200	Thr Pro Pro Val Pro Val Ser Asp Phe Arg Val Thr Val Val Ser Thr			
201	455	460	465	
203	acg gag atc ggc tta gca tgg agc agc cat gat gca gaa tca ttt cag			1798
204	Thr Glu Ile Gly Leu Ala Trp Ser Ser His Asp Ala Glu Ser Phe Gln			
205	470	475	480	
207	atg cat atc aca cag gag gga gct ggc aat tct cgg gta gaa ata acc			1846
208	Met His Ile Thr Gln Glu Gly Ala Gly Asn Ser Arg Val Glu Ile Thr			
209	485	490	495	
211	acc aac caa agt att atc att ggt ggc ttg ttc cct gga acc aag tat			1894
212	Thr Asn Gln Ser Ile Ile Gly Gly Leu Phe Pro Gly Thr Lys Tyr			
213	500	505	510	515
215	tgc ttt gaa ata gtt cca aaa gga cca aat ggg act gaa ggg gca tct			1942
216	Cys Phe Glu Ile Val Pro Lys Gly Pro Asn Gly Thr Glu Gly Ala Ser			
217	520	525	530	
219	cgg aca gtt tgc aat aga act gtt ccc agt gca gtg ttt gac atc cac			1990
220	Arg Thr Val Cys Asn Arg Thr Val Pro Ser Ala Val Phe Asp Ile His			
221	535	540	545	
223	gtg gtc tac gtc acc acc acg gag atg tgg ctg gac tgg aag agc cct			2038
224	Val Val Tyr Val Thr Thr Glu Met Trp Leu Asp Trp Lys Ser Pro			
225	550	555	560	
227	gac ggt gct tcc gag tat gtc tac cat tta gtc ata gag tcc aag cat			2086
228	Asp Gly Ala Ser Glu Tyr Val Tyr His Leu Val Ile Glu Ser Lys His			
229	565	570	575	
231	ggc tct aac cac aca agc acg tat gac aaa gcg att act ctc cag ggc			2134
232	Gly Ser Asn His Thr Ser Thr Tyr Asp Lys Ala Ile Thr Leu Gln Gly			
233	580	585	590	595
235	ctg att ccg ggc acc tta tat aac atc acc atc tct cca gaa gtg gac			2182
236	Leu Ile Pro Gly Thr Leu Tyr Asn Ile Thr Ile Ser Pro Glu Val Asp			
237	600	605	610	
239	cac gtc tgg ggg gac ccc aac tcc act gca cag tac aca cgg ccc agc			2230
240	His Val Trp Gly Asp Pro Asn Ser Thr Ala Gln Tyr Thr Arg Pro Ser			
241	615	620	625	
243	aat gtg tcc aac att gat gta agt acc aac acc aca gca gca act tta			2278
244	Asn Val Ser Asn Ile Asp Val Ser Thr Asn Thr Thr Ala Ala Thr Leu			
245	630	635	640	
247	agt tgg cag aac ttt gat gac gcc tct ccc acg tac tac tgc ctt			2326
248	Ser Trp Gln Asn Phe Asp Asp Ala Ser Pro Thr Tyr Ser Tyr Cys Leu			
249	645	650	655	
251	ctt att gag aag gct gga aat tcc agc aac gca aca caa gta gtc acg			2374
252	Leu Ile Glu Lys Ala Gly Asn Ser Ser Asn Ala Thr Gln Val Val Thr			
253	660	665	670	675
255	gac att gga att act gac gct aca gtc act gaa tta ata cct ggc tca			2422
256	Asp Ile Gly Ile Thr Asp Ala Thr Val Thr Glu Leu Ile Pro Gly Ser			
257	680	685	690	
259	tca tac aca gtg gag atc ttt gca caa gta ggg gat ggg atc aag tca			2470
260	Ser Tyr Thr Val Glu Ile Phe Ala Gln Val Gly Asp Gly Ile Lys Ser			
261	695	700	705	

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263	ctg	gaa	cct	ggc	cg	aag	tca	ttc	tgt	aca	gat	cct	g	cc	tcc	atg	gcc		2518		
264	Leu	Glu	Pro	Gly	Arg	Lys	Ser	Phe	Cys	Thr	Asp	Pro	Ala	Ser	Met	Ala					
265																	720				
266	710																				
267	tcc	ttc	gac	tgc	gaa	gtg	gtc	ccc	aaa	gag	cca	gcc	ctg	gtt	ctc	aaa		2566			
268	Ser	Phe	Asp	Cys	Glu	Val	Val	Pro	Lys	Glu	Pro	Ala	Leu	Val	Leu	Lys					
269																					
270	725																				
271	tgg	acc	tgc	cct	ggc	g	cc	aat	gca	ggc	ttt	gag	ctg	gag	gtc	agc		2614			
272	Trp	Thr	Cys	Pro	Pro	Gly	Ala	Asn	Ala	Gly	Phe	Glu	Leu	Glu	Val	Ser					
273																	755				
274	740																				
275	agt	gga	gcc	tgg	aac	aat	g	cg	acc	cac	ctg	gag	agc	tgc	tcc	tct	gag		2662		
276	Ser	Gly	Ala	Trp	Asn	Asn	Ala	Thr	His	Leu	Glu	Ser	Cys	Ser	Ser	Glu					
277																					
278	760																				
279	aat	ggc	act	gag	tat	aga	acg	gaa	gtc	acg	tat	ttg	aat	ttt	tct	acc		2710			
280	Asn	Gly	Thr	Glu	Tyr	Arg	Thr	Glu	Val	Thr	Tyr	Leu	Asn	Phe	Ser	Thr					
281																	785				
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283	tcg	tac	aa	atc	agc	atc	acc	act	gtg	tcc	tgt	gga	aag	atg	gca	gcc		2758			
284	Ser	Tyr	Asn	Ile	Ser	Ile	Thr	Thr	Val	Ser	Cys	Gly	Lys	Met	Ala	Ala					
285																	800				
286	790																				
287	ccc	acc	cg	g	aa	cc	tgc	act	act	ggc	atc	aca	gat	ccc	cct	cct	cca		2806		
288	Pro	Thr	Arg	Asn	Thr	Cys	Thr	Thr	Gly	Ile	Thr	Asp	Pro	Pro	Pro	Pro					
289																					
290	805																				
291	aat	gg	ta	cc	c	t	aa	t	t	gt	ag	cac	aat	tca	gt	a	gg		2854		
292	Asp	Gly	Ser	Pro	Asn	Ile	Thr	Ser	Val	Ser	His	Asn	Ser	Val	Lys	Val					
293																	835				
294	820																				
295	aag	ttc	agt	gg	ttt	gaa	ggc	agc	cac	gga	ccc	atc	aaa	ggc	tat	gt		2902			
296	Lys	Phe	Ser	Gly	Phe	Glu	Ala	Ser	His	Gly	Pro	Ile	Lys	Ala	Tyr	Ala					
297																	850				
298	840																				
299	gtc	att	ctc	acc	acc	ggg	gaa	gct	ggt	cac	cct	tct	gca	gat	gtc	ctg		2950			
300	Val	Ile	Leu	Thr	Thr	Gly	Glu	Ala	Gly	His	Pro	Ser	Ala	Asp	Val	Leu					
301																	865				
302	855																				
303	aaa	tac	ac	tg	tac	gat	ttc	aaa	aag	gg	cc	tca	gat	act	tat	gt		2998			
304	Lys	Tyr	Th	R	Tyr	Asp	Asp	Phe	Lys	Lys	Gly	Ala	Ser	Asp	Thr	Tyr	Val				
305																	880				
306	870																				
307	aca	tac	ctc	ata	aga	aca	gaa	aag	gg	cgt	tct	cag	agc	ttg	tct		3046				
308	Thr	Tyr	Leu	Ile	Arg	Thr	Glu	Glu	Lys	Gly	Arg	Ser	Gln	Ser	Leu	Ser					
309																	895				
310	885																				
311	gaa	gtt	ttg	aaa	tat	gaa	att	gac	gtt	ggg	aat	gag	tca	acc	aca	ctt		3094			
312	Glu	Val	Leu	Lys	Tyr	Glu	Ile	Asp	Val	Gly	Asn	Glu	Ser	Thr	Thr	Leu					
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314	900																				
315	905																				
316	ggt	tat	ta	gg	aa	g	ct	gt	gg	t	ct	g	at	gt	tg		3142				
317	Gly	Tyr	Tyr	Asn	Gly	Lys	Leu	Glu	Pro	Leu	Gly	Ser	Tyr	Arg	Ala	Cys					
318																	930				
319	920																				
320	gt	g	c	tt	cc	ac	aa	tt	cc	ca	aa	gg	gg	cc	tt	cc		3190			
321	935																945				
322	att	gat	ggg	g	tt	g	ac	t	gt	tc	t	tc	g	at	gt	ct		3238			
323	Ile	Asp	Gly	Ala	Glu	Ser	Tyr	Val	Ser	Phe	Ser	Arg	Tyr	Ser	Asp	Ala					
324																	960				
325	950																				
326	gtt	tcc	ttt	cc	cag	gat	cc	gg	t	tc	t	tc	g	ga	gg	gg		3286			
327																					

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valid <213> Response:

is of "Artificial" only as "<213> Organism" response is incomplete,
r 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

g#:2

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